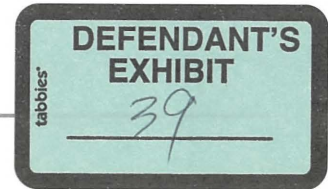


From: [Bryan J Pesta](#)
To: [John Fuerst](#); [Emil O. W. Kirkegaard](#)
Subject: Re: Application for dbgap version 2.3
Date: Tuesday, July 10, 2018 10:18:41 AM



It's fine, but I'm going to change it to say "we Will use..." in various places.

Bryan

From: John Fuerst <j122177@hotmail.com>
Sent: Tuesday, July 10, 2018 10:14:44 AM
To: Bryan J Pesta; Emil O. W. Kirkegaard
Subject: Application for dbgap version 2.3

I altered to meet Bryan and Emil's suggestion :

“Admixture analysis investigation of psychological disorders in an admixed American population.”

In the US, ethnic groups are diagnosed for cognitive/mood disorders such as schizophrenia and depression at different rates. These rate differences have frequently been attributed to diagnostic bias (e.g., Escobar, 2012). However, recent genomic research implicates evolutionary effects in some cases. For example, analyzing polygenic score, Guo et al. (2018) found evidence of natural selection for schizophrenia in context to European, African, and East Asian descent groups both globally and in the United States. As polygenic scores have questionable cross-ethnic validity, there is substantial uncertainty about such results. We utilize Trajectories of Complex Phenotypes to investigate a selection hypothesis using admixture analyses. We employ admixture analysis to determine if global ancestry predicts the likelihood of having a disorder. Since concern has been raised about confounding we control for relevant factors such as socioeconomic status. Additionally, we apply admixture mapping (Shriner, 2013) to determine which regions of the genome are most strongly associate with outcomes.

To maximize statistical power, we use the full sample. Genotypic data is used to ascertain ancestry. We leverage genotypic data to compute ancestry percentages and to identify regions of the genome where associations are prominent. The study will primarily involve regression analyses, looking at the association between ancestry and outcomes. We will use SNP genotypes to create ancestry estimates, along with demographic data (e.g., age, sex, parental SES, etc.) and neuropsychiatric data.

From: Bryan J Pesta <b.pesta@csuohio.edu>
Sent: Tuesday, July 10, 2018 10:45 AM
To: Emil O. W. Kirkegaard; John Fuerst
Subject: Re: Registered Reports to avoid results bias

Guys,

It was great having you over-- hope the accommodations were fine (I don't host much).

I'll look into the RR thing soon, and please let me know which version of the application to submit.

Thanks!

Bryan

From: Emil O. W. Kirkegaard <the.dfx@gmail.com>

Sent: Monday, July 9, 2018 5:52:42 PM

To: John Fuerst; Bryan J Pesta

Subject: Registered Reports to avoid results bias

Guys,

Good to see you in real life. I made it home safely.

I see that a new journal now also takes these RR's as they are called.

<https://onlinelibrary.wiley.com/page/journal/20448295/homepage/registeredreportsguidelines.htm>

Could be an idea to look into journals that take these and see if we can find a way to use this.

--

Emil O. W. Kirkegaard, Ulster Institute for Social Research.

Scientist, etc. - [Google Scholar](#) / [ResearchGate](#).

emilkirkegaard.dk Personal website.